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SEQ ID No. 1.

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 TCGAATGAC ATTGAGATT ATGAGCTT TTGCTGTGA ACGAGAGAT TCTGATAGT 780
 GGGACGATT CTACATTAG GAGGTGAAA AATACAAGT CCTAAAAAT GCTATGTTG 840
 AAGGTGATG CTCAAGCGA AGCTATTCT TGGCTGCTC TGCATTACT GAGGGAGCTG 900
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 TGGAGATGAT GGGAGCGAG GTTACATGA CCGAGACTAG CGTAACTGT ACTGCGCCAC 1020
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 GAGAGCTGC TTCTTGAGA GTTAAGGAG CCGAGAGAT GGTTCGATC CGAGCGGAG 1200
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10023839.122101

SEQ ID N . 2.

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 Arg Val Asn Gly Ile Gly Gly Leu Pro Gly Gly Lys Val Lys Leu Ser
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ATT CCG TAC GTC GAA ATG ACA TTG AGA TTG ATG GAG CGT TTT GGT GTG 671
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10023839.12210.1

SEQ ID No. 2 (continuation).

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AGC GTA ACT GTT ACT GGC CCA CCG CCG GAG CCA TTT GGG ACG AAA CAC Ser Val Thr Val Thr Gly Pro Pro Arg Glu Pro Phe Gly Arg Lys His 305 310 315	959
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CGG ACG GAG CTA ACC AAG CTG GGA GCA TCT GTT GAG GAA GCG CCG GAC Arg Thr Glu Leu Thr Lys Leu Gly Ala Ser Val Glu Glu Gly Pro Asp 370 375 380	1151
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TAA	1340

F0023839.122101

SEQ ID No. 3.

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 Gly Gly Lys Phe Pro Val Glu Asp Ala Lys Glu Glu Val Glu Leu Phe
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 325 330 335
 Ala Val Val Ala Leu Phe Ala Asp Gly Pro Thr Ala Ile Arg Asp Val
 340 345 350
 Ala Ser Trp Arg Val Lys Glu Thr Glu Arg Met Val Ala Ile Arg Thr
 355 360 365
 Glu Leu Thr Lys Leu Gly Ala Ser Val Glu Glu Gly Pro Asp Tyr Cys
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 Ile Ile Thr Pro Pro Glu Lys Leu Asn Val Thr Ala Ile Asp Thr Tyr
 385 390 395 400
 Asp Asp His Arg Met Ala Met Ala Phe Ser Leu Ala Ala Cys Ala Glu
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SEQ ID No. 4.

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Leu	Asn	Ser	Glu	Asp	Val	His	Tyr	Met	Leu	Gly	Ala	Leu	Arg	Thr	Leu	
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CTT	GCT	GCA	GAT	GTT	GAT	TGT	TTC	CTT	GCG	ACT	GAC	TGC	CCA	CCT	GTT	479
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OCT GAG GTA CTG GAG ATG ATG GGA GCG AAG GTT ACA TGG ACC GAG ACT Ala Glu Val Leu Glu Met Met Gly Ala Lys Val Thr Trp Thr Glu Thr 290 295 300	911
AAC GTA ACT GTT ACT GGC CCA CCG CCG GAG CCA TTT GGG AGG AAA CAC Ser Val Thr Val Thr Gly Pro Pro Arg Glu Pro Phe Gly Arg Lys His 305 310 315	959
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CGG ACG GAG CTA ACC AAG CTG GCA CCA TCT GTT GAG GAA GCG CCG GAC Arg Thr Glu Leu Thr Lys Leu Gly Ala Ser Val Glu Glu Gly Pro Asp 370 375 380	1151
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GCC GAG GTC CCC GTC ACC ATC CCG GAC CCT GCG TGC ACC CCG AAG ACC Ala Glu Val Pro Val Thr Ile Arg Asp Pro Gly Cys Thr Arg Lys Thr 415 420 425 430	1295
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TAA	1340

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SEQ ID No. 6.

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F0122T "6E8E200T

SEQ ID No. 7.

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10023839-12101

SEQUENCE LISTING

<110> DEROSE, Richard
CHAUBET, Nicole
GIGOT, Claude (deceased)

<120> ISOLATED DNA SEQUENCE CAPABLE OF SERVING AS REGULATORY
ELEMENT IN A CHIMERIC GENE WHICH CAN BE USED FOR THE
TRANSFORMATION OF PLANTS

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Asn Ser Glu Asp Val His Tyr Met Leu Gly Ala Leu Arg Thr Leu Gly	
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Leu Ser Val Glu Ala Asp Lys Ala Ala Lys Arg Ala Val Val Val Gly	
65 70 75	
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Cys Gly Gly Lys Phe Pro Val Glu Asp Ala Lys Glu Glu Val Gln Leu	
80 85 90 95	
ttc ttg ggg aat gct gga act gca atg cgg cca ttg aca gca gct gtt	338
Phe Leu Gly Asn Ala Gly Thr Ala Met Arg Pro Leu Thr Ala Ala Val	
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act gct gct ggt gga aat gca act tac gtg ctt gat gga gta cca aga	386
Thr Ala Ala Gly Gly Asn Ala Thr Tyr Val Leu Asp Gly Val Pro Arg	
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Met Arg Glu Arg Pro Ile Gly Asp Leu Val Val Gly Leu Lys Gln Leu	
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ggg gca gat gtt gat tgt ttc ctt ggc act gac tgc cca cct gtt cgt	482
Gly Ala Asp Val Asp Cys Phe Leu Gly Thr Asp Cys Pro Pro Val Arg	
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gtc aat gga atc gga ggg cta cct ggt ggc aag gtc aag ctg tct ggc	530
Val Asn Gly Ile Gly Gly Leu Pro Gly Gly Lys Val Lys Leu Ser Gly	
160 165 170 175	
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Ser Ile Ser Ser Gln Tyr Leu Ser Ala Leu Leu Met Ala Ala Pro Leu	
180 185 190	
gct ctt ggg gat gtg gag att gaa atc att gat aaa tta atc tcc att	626
Ala Leu Gly Asp Val Glu Ile Glu Ile Ile Asp Lys Leu Ile Ser Ile	
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ccg tac gtc gaa atg aca ttg aga ttg atg gag cgt ttt ggt gtg aaa	674
Pro Tyr Val Glu Met Thr Leu Arg Leu Met Glu Arg Phe Gly Val Lys	
210 215 220	
gca gag cat tct gat agc tgg gac aga ttc tac att aag gga ggt caa	722
Ala Glu His Ser Asp Ser Trp Asp Arg Phe Tyr Ile Lys Gly Gly Gln	
225 230 235	
aaa tac aag tcc cct aaa aat gcc tat gtt gaa ggt gat gcc tca agc	770
Lys Tyr Lys Ser Pro Lys Asn Ala Tyr Val Glu Gly Asp Ala Ser Ser	
240 245 250 255	
gca agc tat ttc ttg gct ggt gct gca att act gga ggg act gtg act	818

Ala Ser Tyr Phe Leu Ala Gly Ala Ala Ile Thr Gly Gly Thr Val Thr	
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gtg gaa ggt tgt ggc acc acc agt ttg cag ggt gat gtg aag ttt gct	866
Val Glu Gly Cys Gly Thr Thr Ser Leu Gln Gly Asp Val Lys Phe Ala	
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Glu Val Leu Glu Met Met Gly Ala Lys Val Thr Trp Thr Glu Thr Ser	
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gta act gtt act ggc cca ccg cgg gag cca ttt ggg agg aaa cac ctc	962
Val Thr Val Thr Gly Pro Pro Arg Glu Pro Phe Gly Arg Lys His Leu	
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Lys Ala Ile Asp Val Asn Met Asn Lys Met Pro Asp Val Ala Met Thr	
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ctt gct gtg gtt gcc ctc ttt gcc gat ggc ccg aca gcc atc aga gac	1058
Leu Ala Val Val Ala Leu Phe Ala Asp Gly Pro Thr Ala Ile Arg Asp	
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Val Ala Ser Trp Arg Val Lys Glu Thr Glu Arg Met Val Ala Ile Arg	
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acg gag cta acc aag ctg gga gca tct gtt gag gaa ggg ccg gac tac	1154
Thr Glu Leu Thr Lys Leu Gly Ala Ser Val Glu Glu Gly Pro Asp Tyr	
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Cys Ile Ile Thr Pro Pro Glu Lys Leu Asn Val Thr Ala Ile Asp Thr	
385 390 395	
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Tyr Asp Asp His Arg Met Ala Met Ala Phe Ser Leu Ala Ala Cys Ala	
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Glu Val Pro Val Thr Ile Arg Asp Pro Gly Cys Thr Arg Lys Thr Phe	
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Leu Ala Ala Leu Ser Glu Gly Thr Thr Val Val Asp Asn Leu Leu Asn	35	40	45
Ser Glu Asp Val His Tyr Met Leu Gly Ala Leu Arg Thr Leu Gly Leu	50	55	60
Ser Val Glu Ala Asp Lys Ala Ala Lys Arg Ala Val Val Val Gly Cys	65	70	75
Gly Gly Lys Phe Pro Val Glu Asp Ala Lys Glu Glu Val Gln Leu Phe	85	90	95
Leu Gly Asn Ala Gly Thr Ala Met Arg Pro Leu Thr Ala Ala Val Thr	100	105	110
Ala Ala Gly Gly Asn Ala Thr Tyr Val Leu Asp Gly Val Pro Arg Met	115	120	125
Arg Glu Arg Pro Ile Gly Asp Leu Val Val Gly Leu Lys Gln Leu Gly	130	135	140
Ala Asp Val Asp Cys Phe Leu Gly Thr Asp Cys Pro Pro Val Arg Val	145	150	155
Asn Gly Ile Gly Gly Leu Pro Gly Gly Lys Val Lys Leu Ser Gly Ser	165	170	175
Ile Ser Ser Gln Tyr Leu Ser Ala Leu Leu Met Ala Ala Pro Leu Ala	180	185	190
Leu Gly Asp Val Glu Ile Glu Ile Ile Asp Lys Leu Ile Ser Ile Pro	195	200	205
Tyr Val Glu Met Thr Leu Arg Leu Met Glu Arg Phe Gly Val Lys Ala	210	215	220
Glu His Ser Asp Ser Trp Asp Arg Phe Tyr Ile Lys Gly Gly Gln Lys	225	230	235
Tyr Lys Ser Pro Lys Asn Ala Tyr Val Glu Gly Asp Ala Ser Ser Ala	245	250	255
Ser Tyr Phe Leu Ala Gly Ala Ala Ile Thr Gly Gly Thr Val Thr Val	260	265	270
Glu Gly Cys Gly Thr Thr Ser Leu Gln Gly Asp Val Lys Phe Ala Glu	275	280	285
Val Leu Glu Met Met Gly Ala Lys Val Thr Trp Thr Glu Thr Ser Val	290	295	300

Thr Val Thr Gly Pro Pro Arg Glu Pro Phe Gly Arg Lys His Leu Lys
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Ala Ile Asp Val Asn Met Asn Lys Met Pro Asp Val Ala Met Thr Leu
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Ala Val Val Ala Leu Phe Ala Asp Gly Pro Thr Ala Ile Arg Asp Val
340 345 350

Ala Ser Trp Arg Val Lys Glu Thr Glu Arg Met Val Ala Ile Arg Thr
355 360 365

Glu Leu Thr Lys Leu Gly Ala Ser Val Glu Glu Gly Pro Asp Tyr Cys
370 375 380

Ile Ile Thr Pro Pro Glu Lys Leu Asn Val Thr Ala Ile Asp Thr Tyr
385 390 395 400

Asp Asp His Arg Met Ala Met Ala Phe Ser Leu Ala Ala Cys Ala Glu
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Gly Thr Val Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ile Leu
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cta ctc gcc gcc ctg tcc gag ggg aca aca gtg gtt gat aac ctg ctg 146
Leu Leu Ala Ala Leu Ser Glu Gly Thr Thr Val Val Asp Asn Leu Leu
35 40 45

aac agt gag gat gtc cac tac atg ctc ggg gcc ttg agg act ctt ggt 194
Asn Ser Glu Asp Val His Tyr Met Leu Gly Ala Leu Arg Thr Leu Gly
50 55 60

ctc tct gtc gaa gcg gac aaa gct gcc aaa aga gct gta gtt gtt ggc 242

Leu Ser Val Glu Ala Asp Lys Ala Ala Lys Arg Ala Val Val Val Gly	
65 70 75	
tgt ggt gga aag ttc cca gtt gag gat gct aaa gag gaa gtg cag ctc	290
Cys Gly Gly Lys Phe Pro Val Glu Asp Ala Lys Glu Glu Val Gln Leu	
80 85 90 95	
ttc ttg ggg aat gct gga atc gca atg cgg tcc ttg aca gca gct gtt	338
Phe Leu Gly Asn Ala Gly Ile Ala Met Arg Ser Leu Thr Ala Ala Val	
100 105 110	
act gct gct ggt gga aat gca act tac gtg ctt gat gga gta cca aga	386
Thr Ala Ala Gly Gly Asn Ala Thr Tyr Val Leu Asp Gly Val Pro Arg	
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atg agg gag aga ccc att ggc gac ttg gtt gtc gga ttg aag cag ctt	434
Met Arg Glu Arg Pro Ile Gly Asp Leu Val Val Gly Leu Lys Gln Leu	
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Gly Ala Asp Val Asp Cys Phe Leu Gly Thr Asp Cys Pro Pro Val Arg	
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Val Asn Gly Ile Gly Gly Leu Pro Gly Gly Lys Val Lys Leu Ser Gly	
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Ser Ile Ser Ser Gln Tyr Leu Ser Ala Leu Leu Met Ala Ala Pro Leu	
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gct ctt ggg gat gtg gag att gaa atc att gat aaa tta atc tcc att	626
Ala Leu Gly Asp Val Glu Ile Glu Ile Ile Asp Lys Leu Ile Ser Ile	
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Pro Tyr Val Glu Met Thr Leu Arg Leu Met Glu Arg Phe Gly Val Lys	
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Ala Glu His Ser Asp Ser Trp Asp Arg Phe Tyr Ile Lys Gly Gly Gln	
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Lys Tyr Lys Ser Pro Lys Asn Ala Tyr Val Glu Gly Asp Ala Ser Ser	
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Ala Ser Tyr Phe Leu Ala Gly Ala Ala Ile Thr Gly Gly Thr Val Thr	
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Val Glu Gly Cys Gly Thr Thr Ser Leu Gln Gly Asp Val Lys Phe Ala	
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Glu Val Leu Glu Met Met Gly Ala Lys Val Thr Trp Thr Glu Thr Ser	
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Val Thr Val Thr Gly Pro Pro Arg Glu Pro Phe Gly Arg Lys His Leu	
305 310 315	
aag gcg att gat gtc aac atg aac aag atg cct gat gtc gcc atg act	1010
Lys Ala Ile Asp Val Asn Met Asn Lys Met Pro Asp Val Ala Met Thr	
320 325 330 335	
ctt gct gtg gtt gcc ctc ttt gcc gat ggc ccg aca gcc atc aga gac	1058
Leu Ala Val Val Ala Leu Phe Ala Asp Gly Pro Thr Ala Ile Arg Asp	
340 345 350	
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Val Ala Ser Trp Arg Val Lys Glu Thr Glu Arg Met Val Ala Ile Arg	
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acg gag cta acc aag ctg gga gca tct gtt gag gaa ggg ccg gac tac	1154
Thr Glu Leu Thr Lys Leu Gly Ala Ser Val Glu Glu Gly Pro Asp Tyr	
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tgc atc atc acg ccg ccg gag aag ctg aac gtg acg gcg atc gac acg	1202
Cys Ile Ile Thr Pro Pro Glu Lys Leu Asn Val Thr Ala Ile Asp Thr	
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Tyr Asp Asp His Arg Met Ala Met Ala Phe Ser Leu Ala Ala Cys Ala	
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Glu Val Pro Val Thr Ile Arg Asp Pro Gly Cys Thr Arg Lys Thr Phe	
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 35 40 45

Ser Glu Asp Val His Tyr Met Leu Gly Ala Leu Arg Thr Leu Gly Leu
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 Ser Val Glu Ala Asp Lys Ala Ala Lys Arg Ala Val Val Val Gly Cys
 65 70 75 80
 Gly Gly Lys Phe Pro Val Glu Asp Ala Lys Glu Glu Val Gln Leu Phe
 85 90 95
 Leu Gly Asn Ala Gly Ile Ala Met Arg Ser Leu Thr Ala Ala Val Thr
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 Ala Ala Gly Gly Asn Ala Thr Tyr Val Leu Asp Gly Val Pro Arg Met
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 Arg Glu Arg Pro Ile Gly Asp Leu Val Val Gly Leu Lys Gln Leu Gly
 130 135 140
 Ala Asp Val Asp Cys Phe Leu Gly Thr Asp Cys Pro Pro Val Arg Val
 145 150 155 160
 Asn Gly Ile Gly Gly Leu Pro Gly Gly Lys Val Lys Leu Ser Gly Ser
 165 170 175
 Ile Ser Ser Gln Tyr Leu Ser Ala Leu Leu Met Ala Ala Pro Leu Ala
 180 185 190
 Leu Gly Asp Val Glu Ile Glu Ile Ile Asp Lys Leu Ile Ser Ile Pro
 195 200 205
 Tyr Val Glu Met Thr Leu Arg Leu Met Glu Arg Phe Gly Val Lys Ala
 210 215 220
 Glu His Ser Asp Ser Trp Asp Arg Phe Tyr Ile Lys Gly Gly Gln Lys
 225 230 235 240
 Tyr Lys Ser Pro Lys Asn Ala Tyr Val Glu Gly Asp Ala Ser Ser Ala
 245 250 255
 Ser Tyr Phe Leu Ala Gly Ala Ala Ile Thr Gly Gly Thr Val Thr Val
 260 265 270
 Glu Gly Cys Gly Thr Thr Ser Leu Gln Gly Asp Val Lys Phe Ala Glu
 275 280 285
 Val Leu Glu Met Met Gly Ala Lys Val Thr Trp Thr Glu Thr Ser Val
 290 295 300
 Thr Val Thr Gly Pro Pro Arg Glu Pro Phe Gly Arg Lys His Leu Lys
 305 310 315 320
 Ala Ile Asp Val Asn Met Asn Lys Met Pro Asp Val Ala Met Thr Leu
 325 330 335
 Ala Val Val Ala Leu Phe Ala Asp Gly Pro Thr Ala Ile Arg Asp Val

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340

345

350

Ala Ser Trp Arg Val Lys Glu Thr Glu Arg Met Val Ala Ile Arg Thr
355 360 365

Glu Leu Thr Lys Leu Gly Ala Ser Val Glu Glu Gly Pro Asp Tyr Cys
370 375 380

Ile Ile Thr Pro Pro Glu Lys Leu Asn Val Thr Ala Ile Asp Thr Tyr
385 390 395 400

Asp Asp His Arg Met Ala Met Ala Phe Ser Leu Ala Ala Cys Ala Glu
405 410 415

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tttcttgatt atcgattgc aattagggat tttctttggg ttgtgttgga tcttacgata 360
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cgggttttgg cccattccag tttgaaaata aacgtccgtc ttttaagttt gctggatcga 180
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<210> 13
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37

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25

<210> 15
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33

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